

## SEQUENCE LISTING

<110> NODA, Masakuni  
MATSUO, Takanori  
TSUGE, Hiroko

<120> Screening Method

<130> 3011 USOP

<150> PCT/JP03/00111

<151> 2003-01-01

<150> JP 2002-3769

<151> 2002-01-10

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(123)

<223> Partial amino acid sequence of Egr-1 protein which is conserved  
between human, mouse and rat.

<400> 1

Tyr	Gln	Ser	Gln	Leu	Ile	Lys	Pro	Ser	Arg	Met	Arg	Lys	Tyr	Pro	Asn
1				5					10					15	
Arg	Pro	Ser	Lys	Thr	Pro	Pro	His	Glu	Arg	Pro	Tyr	Ala	Cys	Pro	Val
			20					25					30		
Glu	Ser	Cys	Asp	Arg	Arg	Phe	Ser	Arg	Ser	Asp	Glu	Leu	Thr	Arg	His
		35				40						45			
Ile	Arg	Ile	His	Thr	Gly	Gln	Lys	Pro	Phe	Gln	Cys	Arg	Ile	Cys	Met
	50					55					60				
Arg	Asn	Phe	Ser	Arg	Ser	Asp	His	Leu	Thr	Thr	His	Ile	Arg	Thr	His
65					70				75					80	
Thr	Gly	Glu	Lys	Pro	Phe	Ala	Cys	Asp	Ile	Cys	Gly	Arg	Lys	Phe	Ala
			85						90					95	
Arg	Ser	Asp	Glu	Arg	Lys	Arg	His	Thr	Lys	Ile	His	Leu	Arg	Gln	Lys
			100					105						110	
Asp	Lys	Lys	Ala	Asp	Lys	Ser	Val	Val	Ala	Ser					
		115					120								

<210> 2

<211> 543

<212> PRT

<213> Homo sapiens

<400> 2

Met	Ala	Ala	Ala	Lys	Ala	Glu	Met	Gln	Leu	Met	Ser	Pro	Leu	Gln	Ile
1				5				10					15		

Ser	Asp	Pro	Phe	Gly	Ser	Phe	Pro	His	Ser	Pro	Thr	Met	Asp	Asn	Tyr
			20					25					30		
Pro	Lys	Leu	Glu	Glu	Met	Met	Leu	Leu	Ser	Asn	Gly	Ala	Pro	Gln	Phe
		35					40					45			
Leu	Gly	Ala	Ala	Gly	Ala	Pro	Glu	Gly	Ser	Gly	Ser	Asn	Ser	Ser	Ser
	50					55					60				
Ser	Ser	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Asn	Ser	Ser	
65					70					75					80
Ser	Ser	Ser	Ser	Thr	Phe	Asn	Pro	Gln	Ala	Asp	Thr	Gly	Glu	Gln	Pro
				85						90				95	
Tyr	Glu	His	Leu	Thr	Ala	Glu	Ser	Phe	Pro	Asp	Ile	Ser	Leu	Asn	Asn
			100					105					110		
Glu	Lys	Val	Leu	Val	Glu	Thr	Ser	Tyr	Pro	Ser	Gln	Thr	Thr	Arg	Leu
		115					120					125			
Pro	Pro	Ile	Thr	Tyr	Thr	Gly	Arg	Phe	Ser	Leu	Glu	Pro	Ala	Pro	Asn
	130					135					140				
Ser	Gly	Asn	Thr	Leu	Trp	Pro	Glu	Pro	Leu	Phe	Ser	Leu	Val	Ser	Gly
145					150					155					160
Leu	Val	Ser	Met	Thr	Asn	Pro	Pro	Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser
				165					170					175	
Pro	Ala	Ala	Ser	Ser	Ala	Ser	Ala	Ser	Gln	Ser	Pro	Pro	Leu	Ser	Cys
			180					185					190		
Ala	Val	Pro	Ser	Asn	Asp	Ser	Ser	Pro	Ile	Tyr	Ser	Ala	Ala	Pro	Thr
		195					200					205			
Phe	Pro	Thr	Pro	Asn	Thr	Asp	Ile	Phe	Pro	Glu	Pro	Gln	Ser	Gln	Ala
	210					215					220				
Phe	Pro	Gly	Ser	Ala	Gly	Thr	Ala	Leu	Gln	Tyr	Pro	Pro	Pro	Ala	Tyr
225					230					235					240
Pro	Ala	Ala	Lys	Gly	Gly	Phe	Gln	Val	Pro	Met	Ile	Pro	Asp	Tyr	Leu
				245					250					255	
Phe	Pro	Gln	Gln	Gln	Gly	Asp	Leu	Gly	Leu	Gly	Thr	Pro	Asp	Gln	Lys
			260					265					270		
Pro	Phe	Gln	Gly	Leu	Glu	Ser	Arg	Thr	Gln	Gln	Pro	Ser	Leu	Thr	Pro
		275					280					285			
Leu	Ser	Thr	Ile	Lys	Ala	Phe	Ala	Thr	Gln	Ser	Gly	Ser	Gln	Asp	Leu
	290					295					300				
Lys	Ala	Leu	Asn	Thr	Ser	Tyr	Gln	Ser	Gln	Leu	Ile	Lys	Pro	Ser	Arg
305					310					315					320
Met	Arg	Lys	Tyr	Pro	Asn	Arg	Pro	Ser	Lys	Thr	Pro	Pro	His	Glu	Arg
				325					330					335	
Pro	Tyr	Ala	Cys	Pro	Val	Glu	Ser	Cys	Asp	Arg	Arg	Phe	Ser	Arg	Ser
			340					345					350		
Asp	Glu	Leu	Thr	Arg	His	Ile	Arg	Ile	His	Thr	Gly	Gln	Lys	Pro	Phe
		355					360					365			
Gln	Cys	Arg	Ile	Cys	Met	Arg	Asn	Phe	Ser	Arg	Ser	Asp	His	Leu	Thr
	370					375					380				
Thr	His	Ile	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Ala	Cys	Asp	Ile
385					390					395					400
Cys	Gly	Arg	Lys	Phe	Ala	Arg	Ser	Asp	Glu	Arg	Lys	Arg	His	Thr	Lys
				405					410					415	
Ile	His	Leu	Arg	Gln	Lys	Asp	Lys	Lys	Ala	Asp	Lys	Ser	Val	Val	Ala
			420					425					430		
Ser	Ser	Ala	Thr	Ser	Ser	Leu	Ser	Ser	Tyr	Pro	Ser	Pro	Val	Ala	Thr
		435					440					445			
Ser	Tyr	Pro	Ser	Pro	Val	Thr	Thr	Ser	Tyr	Pro	Ser	Pro	Ala	Thr	Thr
	450					455					460				
Ser	Tyr	Pro	Ser	Pro	Val	Pro	Thr	Ser	Phe	Ser	Ser	Pro	Gly	Ser	Ser



gca gtg cca tcc aac gac agc agt ccc att tac tca gcg gca ccc acc	624
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr	
195 200 205	
ttc ccc acg ccg aac act gac att ttc cct gag cca caa agc cag gcc	672
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala	
210 215 220	
ttc ccg ggc tcg gca ggg aca gcg ctc cag tac ccg cct cct gcc tac	720
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr	
225 230 235 240	
cct gcc gcc aag ggt ggc ttc cag gtt ccc atg atc ccc gac tac ctg	768
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu	
245 250 255	
ttt cca cag cag cag ggg gat ctg ggc ctg ggc acc cca gac cag aag	816
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys	
260 265 270	
ccc ttc cag ggc ctg gag agc cgc acc cag cag cct tcg cta acc cct	864
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro	
275 280 285	
ctg tct act att aag gcc ttt gcc act cag tcg ggc tcc cag gac ctg	912
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu	
290 295 300	
aag gcc ctc aat acc agc tac cag tcc cag ctc atc aaa ccc agc cgc	960
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg	
305 310 315 320	
atg cgc aag tat ccc aac cgg ccc agc aag acg ccc ccc cac gaa cgc	1008
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg	
325 330 335	
cct tac gct tgc cca gtg gag tcc tgt gat cgc cgc ttc tcc cgc tcc	1056
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser	
340 345 350	
gac gag ctc acc cgc cac atc cgc atc cac aca ggc cag aag ccc ttc	1104
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe	
355 360 365	
cag tgc cgc atc tgc atg cgc aac ttc agc cgc agc gac cac ctc acc	1152
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr	
370 375 380	
acc cac atc cgc acc cac aca ggc gaa aag ccc ttc gcc tgc gac atc	1200
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile	
385 390 395 400	
tgt gga aga aag ttt gcc agg agc gat gaa cgc aag agg cat acc aag	1248
Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys	
405 410 415	
atc cac ttg cgg cag aag gac aag aaa gca gac aaa agt gtt gtg gcc	1296
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala	
420 425 430	
tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc	1344
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr	
435 440 445	
tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc	1392
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr	
450 455 460	
tca tac cca tcc cct gtg ccc acc tcc ttc tcc tct ccc ggc tcc tcg	1440
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser	
465 470 475 480	
acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc	1488
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala	
485 490 495	

acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc	1536
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser	
500 505 510	
ttc cct tcc tca gct gtc acc aac tcc ttc agc gcc tcc aca ggg ctt	1584
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu	
515 520 525	
tcg gac atg aca gca acc ttt tct ccc agg aca att gaa att tgc	1629
Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys	
530 535 540	

<210> 4  
 <211> 1629  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1629)  
 <223>

<400> 4	
atg gcc gcg gcc aag gcc gag atg cag ctg atg tcc ccg ctg cag atc	48
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile	
1 5 10 15	
tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac	96
Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr	
20 25 30	
cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc	144
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe	
35 40 45	
ctc ggc gcc gcc ggg gcc cca gag ggc agc ggc agc aac agc agc agc	192
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser	
50 55 60	
agc agc agc ggg ggc ggt gga ggc ggc ggg ggc ggc agc aac agc agc	240
Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser	
65 70 75 80	
agc agc agc agc acc ttc aac cct cag gcg gac acg ggc gag cag ccc	288
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro	
85 90 95	
tac gag cac ctg acc gca gag tct ttt cct gac atc tct ctg aac aac	336
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn	
100 105 110	
gag aag gtg ctg gtg gag acc agt tac ccc agc caa acc act cga ctg	384
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu	
115 120 125	
ccc ccc atc acc tat act ggc cgc ttt tcc ctg gag cct gca ccc aac	432
Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn	
130 135 140	
agt ggc aac acc ttg tgg ccc gag ccc ctc ttc agc ttg gtc agt ggc	480
Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly	
145 150 155 160	
cta gtg agc atg acc aac cca ccg gcc tcc tcg tcc tca gca cca tct	528
Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser	
165 170 175	
cca gcg gcc tcc tcc gcc tcc gcc tcc cag agc cca ccc ctg agc tgc	576
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys	
180 185 190	

gca gtg cca tcc aac gac agc agt ccc att tac tca gcg gca ccc acc	624
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr	
195 200 205	
ttc ccc acg ccg aac act gac att ttc cct gag cca caa agc cag gcc	672
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala	
210 215 220	
ttc ccg ggc tcg gca ggg aca gcg ctc cag tac ccg cct cct gcc tac	720
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr	
225 230 235 240	
cct gcc gcc aag ggt ggc ttc cag gtt ccc atg atc ccc gac tac ctg	768
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu	
245 250 255	
ttt cca cag cag cag ggg gat ctg ggc ctg ggc acc cca gac cag aag	816
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys	
260 265 270	
ccc ttc cag ggc ctg gag agc cgc acc cag cag cct tcg cta acc cct	864
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro	
275 280 285	
ctg tct act att aag gcc ttt gcc act cag tcg ggc tcc cag gac ctg	912
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu	
290 295 300	
aag gcc ctc aat acc agc tac cag tcc cag ctc atc aaa ccc agc cgc	960
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg	
305 310 315 320	
atg cgc aag tac ccc aac cgg ccc agc aag acg ccc ccc cac gaa cgc	1008
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg	
325 330 335	
cct tac gct tgc cca gtg gag tcc tgt gat cgc cgc ttc tcc cgc tcc	1056
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser	
340 345 350	
gac gag ctc acc cgc cac atc cgc atc cac aca ggc cag aag ccc ttc	1104
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe	
355 360 365	
cag tgc cgc atc tgc atg cgc aac ttc agc cgc agc gac cac ctc acc	1152
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr	
370 375 380	
acc cac atc cgc acc cac aca ggc gaa aag ccc ttc gcc tgc gac atc	1200
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile	
385 390 395 400	
tgt gga aga aag ttt gcc agg agc gat gaa cgc aag agg cat acc aag	1248
Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys	
405 410 415	
atc cac ttg cgg cag aag gac aag aaa gca gac aaa agt gtt gtg gcc	1296
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala	
420 425 430	
tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc	1344
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr	
435 440 445	
tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc	1392
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr	
450 455 460	
tca tac cca tcc cct gtg ccc acc tcc ttc tcc tct ccc ggc tcc tcg	1440
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser	
465 470 475 480	
acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc	1488
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala	
485 490 495	

acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc	1536
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser	
500 505 510	
ttc cct tcc tca gct gtc acc aac tcc ttc agc gcc tcc aca ggg ctt	1584
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu	
515 520 525	
tcg gac atg aca gca acc ttt tct ccc agg aca att gaa att tgc	1629
Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys	
530 535 540	

<210> 5  
 <211> 9  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligonucleotide designed to act as decoy for Egr-1.

<400> 5  
 gcgtgggacg 9

<210> 6  
 <211> 9  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligonucleotide designed to act as decoy for Egr-1.

<400> 6  
 gcgggggacg 9

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligonucleotide designed to act as antisense DNA for Egr-1 mRNA.

<400> 7  
 gcgggggtgca ggggcacact 20

<210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligonucleotide designed to act as primer for amplifying Egr-1 cDNA.

<400> 8  
 ccgaattcag tgttccccgc gccccgcatg 30

<210> 9  
 <211> 29

<212> DNA  
<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying Egr-1 cDNA.

<400> 9

ggctcgagaa cctccatctg acctaagag

29

<210> 10

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as sense strand of double-stranded DNA capable of binding with Egr-1.

<400> 10

tgactcgccc tcgcccccgcc gccggg

26

<210> 11

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as sense strand of double-stranded DNA incapable of binding with Egr-1.

<400> 11

tgactcgccc tcgaccacgc gccggg

26